



```

name: <unnamed>
log: C:\Users\kamcd\Dropbox\CDK WORK\racial disparities essentialism\JOP repli
> cation files\Anoll Kam Marcellin ANES 2022 Pilot Analyses.smcl
log type: smcl
opened on: 10 Jan 2025, 13:26:19

```

```

1 .
2 . clear

3 . cd "C:\Users\kamcd\Dropbox\CDK WORK\racial disparities essentialism\JOP replication
> files"
C:\Users\kamcd\Dropbox\CDK WORK\racial disparities essentialism\JOP replication files

4 . use "Anoll Kam Marcellin ANES 2022 Pilot Data", clear

5 . svyset [pweight=weight]

Sampling weights: weight
                  VCE: linearized
                  Single unit: missing
                  Strata 1: <one>
                  Sampling unit 1: <observations>
                  FPC 1: <zero>

6 . set scheme slmono

7 .
8 . *****RACE OF RESPONDENT AND PARTY OF WHITES*****
9 . *generate categorical variables for respondents
10. gen fivegroups = .
    (1,585 missing values generated)

11. replace fivegroups = 1 if ras==1|rpi==1
    (67 real changes made)

12. replace fivegroups = 2 if rbl==1
    (211 real changes made)

13. replace fivegroups = 3 if rwh==1 & eth==1
    (182 real changes made)

14. replace fivegroups = 4 if rwh==1 & pid7>0 & pid7<4
    (460 real changes made)

15. replace fivegroups = 5 if rwh==1 & pid7>4 & pid7<8
    (531 real changes made)

16. lab def fivegroups 1"Asian" 2"Black" 3"Hispanic" 4"White DEM" 5"White GOP"

17. lab val fivegroups fivegroups

18. tab fivegroups

```

fivegroups	Freq.	Percent	Cum.
Asian	58	4.43	4.43
Black	203	15.51	19.94
Hispanic	57	4.35	24.29
White DEM	460	35.14	59.43
White GOP	531	40.57	100.00
Total	1,309	100.00	

```

19.
20. *level of nonresponse*
21. egen gdiff_miss = anycount(gdiffbiol gdiffculture gdiffpolicy), val(-7)
22. tab gdiff_miss

```

gdiffbiol gdiffcultur e gdiffpolicy == -7	Freq.	Percent	Cum.
0	1,582	99.81	99.81
1	1	0.06	99.87
3	2	0.13	100.00
Total	1,585	100.00	

```

23. /*Most people answered these questions*/
24. /*1 person refused one of the questions; 2 people skipped the entire battery*/
25. /*1582 people answered ALL of them*/
26.
27. //Analogous to first set of analyses, proportion agreeing with >1 Q
28. recode gdiffbiol (1/4=0) (5=1) (else=.), gen(NOT_bio)
    (1,585 differences between gdiffbiol and NOT_bio)
29. recode gdiffculture (1/4=0) (5=1) (else=.), gen(NOT_cul)
    (1,585 differences between gdiffculture and NOT_cul)
30. recode gdiffpolicy (1/4=0) (5=1) (else=.), gen(NOT_pol)
    (1,585 differences between gdiffpolicy and NOT_pol)
31.
32. gen YES_bio = -1*(NOT_bio-1)
    (3 missing values generated)
33. gen YES_cul = -1*(NOT_cul-1)
    (2 missing values generated)
34. gen YES_pol = -1*(NOT_pol-1)
    (2 missing values generated)
35.
36. egen number_agree = anycount(YES_bio YES_cul YES_pol), val(1)
37. recode number_agree (1 2 3=1) (0=0) (else=.), gen(any_agree)
    (1,217 differences between number_agree and any_agree)
38. tab number_agree

```

YES_bio YES_cul YES_pol == 1	Freq.	Percent	Cum.
0	139	8.77	8.77
1	229	14.45	23.22
2	466	29.40	52.62
3	751	47.38	100.00
Total	1,585	100.00	

39. svy: reg any_agree i.fivegroups
 (running **regress** on estimation sample)

Survey: Linear regression

Number of strata =	1	Number of obs =	1,236
Number of PSUs =	1,236	Population size =	1,236.7822
		Design df =	1,235
		F(4, 1232) =	15.46
		Prob > F =	0.0000
		R-squared =	0.0539

any_agree	Coefficient	Linearized std. err.	t	P> t	[95% conf. interval]	
fivegroups						
Black	-.0344671	.023756	-1.45	0.147	-.0810738	.0121396
Hispanic	-.1094787	.0511247	-2.14	0.032	-.2097794	-.0091779
White DEM	.001435	.0182745	0.08	0.937	-.0344175	.0372875
White GOP	-.1441516	.0246647	-5.84	0.000	-.1925409	-.0957623
_cons	.9774108	.0168228	58.10	0.000	.9444064	1.010415

40.
 41. drop if any_agree==0 /*disputing the underlying premise of the Q*/
 (139 observations deleted)

42.
 43. recode gdifffbiol (1=1) (2=.75) (3=.5) (4=.25) (5=0) (else=.), gen(diff_bio)
 (1,340 differences between **gdifffbiol** and **diff_bio**)
 44. recode gdifffculture (1=1) (2=.75) (3=.5) (4=.25) (5=0) (else=.), gen(diff_cul)
 (1,267 differences between **gdifffculture** and **diff_cul**)
 45. recode gdifffpolicy (1=1) (2=.75) (3=.5) (4=.25) (5=0) (else=.), gen(diff_pol)
 (1,071 differences between **gdifffpolicy** and **diff_pol**)

46.
 47. *****in text
 48. svy: tab YES_bio
 (running **tabulate** on estimation sample)

Number of strata =	1	Number of obs =	1,364
Number of PSUs =	1,364	Population size =	1,368.3561
		Design df =	1,363

YES_bio	proportion
0	.4017
1	.5983
Total	1

Key: proportion = **Cell proportion**

49. svy: tab YES_cul
 (running **tabulate** on estimation sample)

Number of strata =	1	Number of obs =	1,365
Number of PSUs =	1,365	Population size =	1,368.8991
		Design df =	1,364

YES_cul	proportion
0	.0882
1	.9118
Total	1

Key: proportion = **Cell proportion**

50. svy: tab YES_pol
(running **tabulate** on estimation sample)

Number of strata = 1
Number of PSUs = 1,365

Number of obs = 1,365
Population size = 1,368.8991
Design df = 1,364

YES_pol	proportion
0	.1294
1	.8706
Total	1

Key: proportion = **Cell proportion**

51. svy: tab fivegroups YES_bio, row
(running **tabulate** on estimation sample)

Number of strata = 1
Number of PSUs = 1,122

Number of obs = 1,122
Population size = 1,124.5519
Design df = 1,121

fivegroups	YES_bio		Total
	0	1	
Asian	.2321	.7679	1
Black	.3043	.6957	1
Hispanic	.192	.808	1
White DE	.5207	.4793	1
White GO	.4192	.5808	1
Total	.4135	.5865	1

Key: **Row proportion**

Pearson:

Uncorrected chi2(4) = 50.0223
Design-based F(3.73, 4178.43) = 8.1098 P = 0.0000

52.
53. *****START FIGURE 1*****
54. gen gdiff1 = gdiffbiol
55. gen gdiff2 = gdiffculture
56. gen gdiff3 = gdiffpolicy

```

57.
58. forval v = 1/3 {
    2. recode gdifff`v' (1=1) (2 3 4 5=0) (else=.), gen(gdifffgreatdeal`v')
    3. }
(1,340 differences between gdifff1 and gdifffgreatdeal1)
(1,267 differences between gdifff2 and gdifffgreatdeal2)
(1,071 differences between gdifff3 and gdifffgreatdeal3)

59.
60. forval v = 1/3 {
    2. recode gdifff`v' (2=1) (1 3 4 5=0) (else=.), gen(gdifffalot`v')
    3. }
(1,446 differences between gdifff1 and gdifffalot1)
(1,446 differences between gdifff2 and gdifffalot2)
(1,446 differences between gdifff3 and gdifffalot3)

61.
62. forval v = 1/3 {
    2. recode gdifff`v' (3=1) (1 2 4 5=0) (else=.), gen(gdifffmoderate`v')
    3. }
(1,446 differences between gdifff1 and gdifffmoderate1)
(1,446 differences between gdifff2 and gdifffmoderate2)
(1,446 differences between gdifff3 and gdifffmoderate3)

63.
64. forval v = 1/3 {
    2. recode gdifff`v' (4=1) (1 2 3 5=0) (else=.), gen(gdifffalittle`v')
    3. }
(1,446 differences between gdifff1 and gdifffalittle1)
(1,446 differences between gdifff2 and gdifffalittle2)
(1,446 differences between gdifff3 and gdifffalittle3)

65.
66. %% FOR FULL SAMPLE
67. foreach j in greatdeal alot moderate alittle {
    2. preserve
    3. collapse gdifff`j'1-gdifff`j'3 [pweight=weight]
    4. gen id = _n
    5. reshape long gdifff`j', i(id) j(Q)
    6. lab def Q 1 "Biology" 2 "Culture" 3 "Politics"
    7. lab val Q Q
    8. sum
    9. gen gdifff`j'percent = gdifff`j'*100
    10. save gdifff`j'percent, replace
    11. restore
    12. }
(j = 1 2 3)

```

Data	Wide	->	Long
Number of observations	1	->	3
Number of variables	4	->	3
j variable (3 values)		->	Q
xij variables:			
gdifffgreatdeal1 gdifffgreatdeal2 gdifffgreatdeal3->gdifffgreatdeal			

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdifffgreatdeal	3	.1474262	.0903339	.07303	.2479419

(file **gdifffgreatdealpercent.dta** not found)
file **gdifffgreatdealpercent.dta** saved
(j = 1 2 3)

```
Data
Wide -> Long
Number of observations 1 -> 3
Number of variables 4 -> 3
j variable (3 values) -> Q
xij variables:
    gdiffalot1 gdiffalot2 gdiffalot3 -> gdiffalot
```

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffalot	3	.1539375	.0391372	.1104044	.18621

(file **gdiffalotpercent.dta** not found)
file **gdiffalotpercent.dta** saved
(j = 1 2 3)

```
Data
Wide -> Long
Number of observations 1 -> 3
Number of variables 4 -> 3
j variable (3 values) -> Q
xij variables:
    gdiffmoderate1 gdiffmoderate2 gdiffmoderate3-> gdiffmoderate
```

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffmoderate	3	.3062812	.0628429	.2576014	.3772252

(file **gdiffmoderatepercent.dta** not found)
file **gdiffmoderatepercent.dta** saved
(j = 1 2 3)

```
Data
Wide -> Long
Number of observations 1 -> 3
Number of variables 4 -> 3
j variable (3 values) -> Q
xij variables:
    gdiffalittle1 gdiffalittle2 gdiffalittle3 -> gdiffalittle
```

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffalittle	3	.1859334	.036499	.1572941	.2270302

(file **gdiffalittlepercent.dta** not found)
file **gdiffalittlepercent.dta** saved

```
68.
69. // % BY FIVEGROUPS
70. forval v=1/5 {
    2. foreach j in greatdeal alot moderate alittle {
    3.     preserve
    4.     collapse gdiff`j'1-gdiff`j'3 [pweight=weight] if fivegroups==`v'
    5.     gen id = _n
    6.     reshape long gdiff`j', i(id) j(Q)
    7.     lab def Q 1 "Biology" 2 "Culture" 3 "Politics"
    8.     lab val Q Q
    9.     sum
    10.    gen gdiff`j'percent_`v' = gdiff`j'*100
    11.    save gdiff`j'percent_`v', replace
    12.    restore
    13.    }
    14.    }
(j = 1 2 3)
```

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffgreatdeal1 gdiffgreatdeal2 gdiffgreatdeal3->gdiffgreatdeal

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffgreat~l	3	.0862266	.0459541	.034336	.1217791

(file **gdiffgreatdealpercent_1.dta** not found)
 file **gdiffgreatdealpercent_1.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffalot1 gdiffalot2 gdiffalot3 -> gdiffalot

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffalot	3	.2088287	.0249665	.1938594	.2376503

(file **gdiffalotpercent_1.dta** not found)
 file **gdiffalotpercent_1.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffmoderate1 gdiffmoderate2 gdiffmoderate3-> gdiffmoderate

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffmoder~e	3	.3822024	.0627041	.3432435	.454535

(file **gdiffmoderatepercent_1.dta** not found)
 file **gdiffmoderatepercent_1.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffalittle1 gdiffalittle2 gdiffalittle3 -> gdiffalittle

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffalittle	3	.1948619	.045619	.1513529	.2423326

(file **gdiffalittlepercent_1.dta** not found)
 file **gdiffalittlepercent_1.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffgreatdeal1 gdiffgreatdeal2 gdiffgreatdeal3->gdiffgreatdeal

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffgreat~l	3	.2998124	.1422224	.1841514	.4586088

(file **gdiffgreatdealpercent_2.dta** not found)
 file **gdiffgreatdealpercent_2.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffalot1 gdiffalot2 gdiffalot3 -> gdiffalot

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffalot	3	.1908883	.0138191	.1767272	.2043379

(file **gdiffalotpercent_2.dta** not found)
 file **gdiffalotpercent_2.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffmoderate1 gdiffmoderate2 gdiffmoderate3-> gdiffmoderate

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffmoder~e	3	.2859017	.0279439	.2675598	.3180627

(file **gdiffmoderatepercent_2.dta** not found)
 file **gdiffmoderatepercent_2.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffalittle1 gdiffalittle2 gdiffalittle3 -> gdiffalittle

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffalittle	3	.0759599	.0429258	.038072	.1225807

(file **gdiffalittlepercent_2.dta** not found)
 file **gdiffalittlepercent_2.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffgreatdeal1 gdiffgreatdeal2 gdiffgreatdeal3->gdiffgreatdeal

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffgreat~l	3	.0552296	.037832	.0258507	.0979176

(file **gdiffgreatdealpercent_3.dta** not found)
 file **gdiffgreatdealpercent_3.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffalot1 gdiffalot2 gdiffalot3 -> gdiffalot

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffalot	3	.1398172	.0699696	.0630571	.2000298

(file **gdiffalotpercent_3.dta** not found)
 file **gdiffalotpercent_3.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffmoderatel gdiffmoderate2 gdiffmoderate3-> gdiffmoderate

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffmoder~e	3	.4624401	.0386152	.4239093	.5011392

(file **gdiffmoderatepercent_3.dta** not found)
 file **gdiffmoderatepercent_3.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffalittle1 gdiffalittle2 gdiffalittle3 -> gdiffalittle

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffalittle	3	.217866	.0393125	.1782326	.2568495

(file **gdiffalittlepercent_3.dta** not found)
 file **gdiffalittlepercent_3.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdifffgreatdeal1 gdifffgreatdeal2 gdifffgreatdeal3->gdifffgreatdeal

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdifffgreat~l	3	.196559	.1824469	.063928	.4046265

(file **gdifffgreatdealpercent_4.dta** not found)
 file **gdifffgreatdealpercent_4.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffalot1 gdiffalot2 gdiffalot3 -> gdiffalot

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffalot	3	.1724152	.068323	.1087933	.244627

(file **gdiffalotpercent_4.dta** not found)
 file **gdiffalotpercent_4.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffmoderatel gdiffmoderate2 gdiffmoderate3-> gdiffmoderate

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffmoder~e	3	.2592422	.087694	.1904394	.3579854

(file **gdiffmoderatepercent_4.dta** not found)
 file **gdiffmoderatepercent_4.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffalittle1 gdiffalittle2 gdiffalittle3 -> gdiffalittle

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffalittle	3	.1424449	.0807212	.0781834	.2330457

(file **gdiffalittlepercent_4.dta** not found)
 file **gdiffalittlepercent_4.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffgreatdeal1 gdiffgreatdeal2 gdiffgreatdeal3->gdiffgreatdeal

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffgreat~l	3	.0497043	.0214945	.0277781	.0707394

(file **gdiffgreatdealpercent_5.dta** not found)
 file **gdiffgreatdealpercent_5.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffalot1 gdiffalot2 gdiffalot3 -> gdiffalot

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffalot	3	.1142626	.0673629	.0655115	.1911287

(file **gdiffalotpercent_5.dta** not found)
 file **gdiffalotpercent_5.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffmoderate1 gdiffmoderate2 gdiffmoderate3-> gdiffmoderate

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffmoder~e	3	.2967645	.0672821	.244019	.3725368

(file **gdiffmoderatepercent_5.dta** not found)
 file **gdiffmoderatepercent_5.dta** saved
 (j = 1 2 3)

Data Wide -> Long

Number of observations 1 -> 3
 Number of variables 4 -> 3
 j variable (3 values) -> Q
 xij variables:
gdiffalittle1 gdiffalittle2 gdiffalittle3 -> gdiffalittle

Variable	Obs	Mean	Std. dev.	Min	Max
id	3	1	0	1	1
Q	3	2	1	1	3
gdiffalittle	3	.2878656	.0384403	.2435051	.3113753

(file **gdiffalittlepercent_5.dta** not found)
 file **gdiffalittlepercent_5.dta** saved

```

71.
72. //PLOTING % FULL SAMPLE
73. preserve

74. clear

75. use gdiffgreatdealpercent, clear

76. merge 1:1 Q using gdiffalotpercent
    (label Q already defined)

```

Result	Number of obs	
Not matched	0	
Matched	3	(_merge==3)

```

77. merge 1:1 Q using gdiffmoderatepercent, gen(merge3)
    (label Q already defined)

```

Result	Number of obs	
Not matched	0	
Matched	3	(merge3==3)

```

78. merge 1:1 Q using gdiffalittlepercent, gen(merge4)
    (label Q already defined)

```

Result	Number of obs	
Not matched	0	
Matched	3	(merge4==3)

```

79. recode Q (1=1 "Biology") (2=2 "Culture") (3=3 "Racist Policies"), gen(graphorder)
    (0 differences between Q and graphorder)

```

```

80. graph hbar gdiffgreatdealpercent gdiffalotpercent gdiffmoderatepercent gdiffalittlep
> ercent, over(graphorder) ///
> name(gdiff_all, replace) ///
> title("All Respondents", size(medium)) ytitle(" ") xsize(5) ysize(4) graphregion(mar
> gin(1+10)) stack asyvars legend(lab(1 "%A Great" "Deal") lab(2 "%A Lot") lab(3 "%Mod
> erate" "Amount") lab(4 "%A Little") symxsize(5) keygap(.5) row(1) forcesize span)

```

```
81. restore
```

```
82.
```

```
83. //PLOTING % FIVE SUBGROUPS
```

```

84. forval v=1/5 {
    2. preserve
    3. use gdiffgreatdealpercent `v', clear
    4.     gen str10 group`v' = "Asian" if `v'==1
    5.     replace group`v' = "Black" if `v'==2
    6.     replace group`v' = "Latino" if `v'==3
    7.     replace group`v' = "White DEM" if `v'==4
    8.     replace group`v' = "White GOP" if `v'==5
    9.     local h = group`v'
    10. merge 1:1 Q using gdiffalotpercent `v'
    11. merge 1:1 Q using gdiffmoderatepercent `v', gen(merge3)
    12. merge 1:1 Q using gdiffalittlepercent `v', gen(merge4)
    13. recode Q (1=1 "Biology") (2=2 "Culture") (3=3 "Racist Policies"), gen(graphorder)
    14. graph hbar gdiffgreatdealpercent gdiffalotpercent gdiffmoderatepercent gdiffalitt
> lepercent, over(graphorder) ///
> name(gdiff_`v', replace) ///
> title("`h' Respondents", size(medium)) ytitle(" ") xsize(5) ysize(4) graphregion(mar
> gin(1+10)) stack asyvars legend(lab(1 "%A Great" "Deal") lab(2 "%A Lot") lab(3 "%Mod
> erate" "Amount") lab(4 "%A Little") symxsize(5) keygap(.5) row(1) forcesize span siz
> e(vvsmall))
    15. restore
    16. }
(0 real changes made)

```

(0 real changes made)
 (0 real changes made)
 (0 real changes made)
 (label **Q** already defined)

Result	Number of obs	
Not matched	0	
Matched	3	(_merge ==3)

(label **Q** already defined)

Result	Number of obs	
Not matched	0	
Matched	3	(merge3 ==3)

(label **Q** already defined)

Result	Number of obs	
Not matched	0	
Matched	3	(merge4 ==3)

(0 differences between **Q** and **graphorder**)
 (note: named style **vvsmall** not found in class **gsize**, default attributes used)
 (3 missing values generated)
 (3 real changes made)
 (0 real changes made)
 (0 real changes made)
 (0 real changes made)
 (label **Q** already defined)

Result	Number of obs	
Not matched	0	
Matched	3	(_merge ==3)

(label **Q** already defined)

Result	Number of obs	
Not matched	0	
Matched	3	(merge3 ==3)

(label **Q** already defined)

Result	Number of obs	
Not matched	0	
Matched	3	(merge4 ==3)

(0 differences between **Q** and **graphorder**)
 (note: named style **vvsmall** not found in class **gsize**, default attributes used)
 (3 missing values generated)
 (0 real changes made)
 (3 real changes made)
 (0 real changes made)
 (0 real changes made)
 (label **Q** already defined)

Result	Number of obs	
Not matched	0	
Matched	3	(_merge ==3)

(label **Q** already defined)

Result	Number of obs
Not matched	0
Matched	3 (merge3==3)

(label **Q** already defined)

Result	Number of obs
Not matched	0
Matched	3 (merge4==3)

(0 differences between **Q** and **graphorder**)
 (note: named style **vvsmall** not found in class **gsize**, default attributes used)
 (3 missing values generated)
 (0 real changes made)
 (0 real changes made)
 (3 real changes made)
 (0 real changes made)
 (label **Q** already defined)

Result	Number of obs
Not matched	0
Matched	3 (_merge==3)

(label **Q** already defined)

Result	Number of obs
Not matched	0
Matched	3 (merge3==3)

(label **Q** already defined)

Result	Number of obs
Not matched	0
Matched	3 (merge4==3)

(0 differences between **Q** and **graphorder**)
 (note: named style **vvsmall** not found in class **gsize**, default attributes used)
 (3 missing values generated)
 (0 real changes made)
 (0 real changes made)
 (0 real changes made)
 (3 real changes made)
 (label **Q** already defined)

Result	Number of obs
Not matched	0
Matched	3 (_merge==3)

(label **Q** already defined)

Result	Number of obs
Not matched	0
Matched	3 (merge3==3)

(label **Q** already defined)

Result	Number of obs
Not matched	0
Matched	3 (merge4==3)

(0 differences between **Q** and **graphorder**)
 (note: named style **vvsmall** not found in class **gsize**, default attributes used)

```

85.
86. graph combine gdiff_all gdiff_1 gdiff_2 gdiff_3 gdiff_4 gdiff_5, row(2) ///
> title("On average, racial groups differ in outcomes...", size(medsmall)) ///
> subtitle("To what extent do you believe these differences are due to...", size(small)
> ) ///
> xsize(6.5) ysize(4) imargin(medlarge) iscale(.425) ycommon xcommon
(note: named style vvsmall not found in class gsize, default attributes used)
(note: named style vvsmall not found in class gsize, default attributes used)
(note: named style vvsmall not found in class gsize, default attributes used)
(note: named style vvsmall not found in class gsize, default attributes used)
87. graph export AppendixFigureC1.pdf, replace
file AppendixFigureC1.pdf saved as PDF format

```

```

88.
89. *****N's for caption*****
90. sum gdiffbiol gdiffculture gdiffpolicy

```

Variable	Obs	Mean	Std. dev.	Min	Max
gdiffbiol	1,446	3.753804	1.321202	-7	5
gdiffculture	1,446	2.988243	1.131126	1	5
gdiffpolicy	1,446	2.73444	1.343966	1	5

```

91. tab fivegroups

```

fivegroups	Freq.	Percent	Cum.
Asian	56	4.69	4.69
Black	191	16.01	20.70
Hispanic	48	4.02	24.73
White DEM	450	37.72	62.45
White GOP	448	37.55	100.00
Total	1,193	100.00	

```

92. *****END FIGURE 1*****
93.
94. *****cleaning up directory*****
95. forval v=1/5 {
2. erase gdiffalittlepercent_`v'.dta
3. erase gdiffmoderatepercent_`v'.dta
4. erase gdiffalotpercent_`v'.dta
5. erase gdiffgreatdealpercent_`v'.dta
6. }
96. erase gdiffalittlepercent.dta
97. erase gdiffmoderatepercent.dta
98. erase gdiffalotpercent.dta
99. erase gdiffgreatdealpercent.dta
100 *****cleaning up directory*****
101
102
103 // % AGREE WITH >1
104 egen diff_agree = anycount(NOT_bio NOT_cul NOT_pol), val(0)

```

105 svy: tab diff_agree
 (running **tabulate** on estimation sample)

Number of strata = 1
 Number of PSUs = 1,365

Number of obs = 1,365
 Population size = 1,368.8991
 Design df = 1,364

NOT_bio NOT_cul NOT_pol == 0	proportion
1	.1557
2	.3081
3	.5362
Total	1

Key: proportion = **Cell proportion**

106 recode diff_agree (0 1=0) (2 3=1) (else=.), gen(morethanone)
 (1,446 differences between **diff_agree** and **morethanone**)

107
 108 *"Conflicting" factors: biology & policy*
 109 svy: tab YES_bio YES_pol
 (running **tabulate** on estimation sample)

Number of strata = 1
 Number of PSUs = 1,364

Number of obs = 1,364
 Population size = 1,368.3561
 Design df = 1,363

YES_bio	YES_pol		Total
	0	1	
0	.0761	.3256	.4017
1	.0533	.545	.5983
Total	.1294	.8706	1

Key: **Cell proportion**

Pearson:

Uncorrected chi2(1) = 29.3155
 Design-based F(1, 1363) = 22.8666 P = 0.0000

110
 111 foreach y of varlist morethanone YES_bio YES_cul YES_pol {
 2. svy: tab `y' fivegroups, col
 3. }
 (running **tabulate** on estimation sample)

Number of strata = 1
 Number of PSUs = 1,123

Number of obs = 1,123
 Population size = 1,125.0949
 Design df = 1,122

RECODE of diff_agree e (NOT_bio NOT_cul NOT_pol == 0)	fivegroups						Total
	Asian	Black	Hispanic	White DE	White GO		
0	.0799	.106	.097	.1295	.2287	.1564	
1	.9201	.894	.903	.8705	.7713	.8436	
Total	1	1	1	1	1	1	

Key: **Column proportion**

Pearson:
 Uncorrected chi2(4) = 26.3167
 Design-based F(3.95, 4435.93) = 5.3261 P = 0.0003
 (running **tabulate** on estimation sample)

Number of strata = 1
 Number of PSUs = 1,122

Number of obs = 1,122
 Population size = 1,124.5519
 Design df = 1,121

YES_bio	fivegroups					Total
	Asian	Black	Hispanic	White DE	White GO	
0	.2321	.3043	.192	.5207	.4192	.4135
1	.7679	.6957	.808	.4793	.5808	.5865
Total	1	1	1	1	1	1

Key: **Column proportion**

Pearson:
 Uncorrected chi2(4) = 50.0223
 Design-based F(3.73, 4178.43) = 8.1098 P = 0.0000
 (running **tabulate** on estimation sample)

Number of strata = 1
 Number of PSUs = 1,123

Number of obs = 1,123
 Population size = 1,125.0949
 Design df = 1,122

YES_cul	fivegroups					Total
	Asian	Black	Hispanic	White DE	White GO	
0	.0539	.1111	.0787	.124	.0569	.0912
1	.9461	.8889	.9213	.876	.9431	.9088
Total	1	1	1	1	1	1

Key: **Column proportion**

Pearson:
 Uncorrected chi2(4) = 13.1228
 Design-based F(3.92, 4402.65) = 2.7000 P = 0.0300
 (running **tabulate** on estimation sample)

Number of strata = 1
 Number of PSUs = 1,123

Number of obs = 1,123
 Population size = 1,125.0949
 Design df = 1,122

YES_pol	fivegroups					Total
	Asian	Black	Hispanic	White DE	White GO	
0	.0977	.0269	.1033	.0433	.2781	.1312
1	.9023	.9731	.8967	.9567	.7219	.8688
Total	1	1	1	1	1	1

Key: **Column proportion**

Pearson:
 Uncorrected chi2(4) = 122.5387
 Design-based F(3.92, 4396.14) = 22.8431 P = 0.0000

```

112
113 *****START FIGURE 2*****
114 gen YES_biopol = .
    (1,446 missing values generated)
115 replace YES_biopol =1 if YES_bio==1 & YES_pol==1
    (764 real changes made)
116 replace YES_biopol =0 if YES_bio==1 & YES_pol==0
    (68 real changes made)
117 replace YES_biopol =0 if YES_bio==0 & YES_pol==1
    (502 real changes made)
118 replace YES_biopol =0 if YES_bio==0 & YES_pol==0
    (111 real changes made)
119
120 tempname memhold
121 tempfile morethanone_any
122 postfile `memhold' fivegroups propagree seprop using morethanone_any, replace
    (file morethanone_any.dta not found)
123 forval v=1/5 {
    2.      svy: reg morethanone if fivegroups==`v'
    3.      post `memhold ' (`v') (_b[_cons]) (_se[_cons])
    4. }
    (running regress on estimation sample)

```

Survey: Linear regression

Number of strata = 1	Number of obs = 55
Number of PSUs = 55	Population size = 66.3357
	Design df = 54
	<u>F(0, 54)</u> = .
	Prob > F = .
	R-squared = 0.0000

morethanone	Coefficient	Linearized std. err.	t	P> t	[95% conf. interval]	
_cons	.9200943	.0337631	27.25	0.000	.8524034	.9877853

(running **regress** on estimation sample)

Survey: Linear regression

Number of strata = 1	Number of obs = 178
Number of PSUs = 178	Population size = 185.3122
	Design df = 177
	<u>F(0, 177)</u> = .
	Prob > F = .
	R-squared = 0.0000

morethanone	Coefficient	Linearized std. err.	t	P> t	[95% conf. interval]	
_cons	.8940172	.0260728	34.29	0.000	.8425636	.9454709

(running **regress** on estimation sample)

Survey: Linear regression

Number of strata = 1
 Number of PSUs = 48

Number of obs = 48
 Population size = 62.3657
 Design df = 47
 F(0, 47) = .
 Prob > F = .
 R-squared = 0.0000

morethanone	Coefficient	Linearized std. err.	t	P> t	[95% conf. interval]	
_cons	.9030413	.044358	20.36	0.000	.8138046	.9922779

(running **regress** on estimation sample)

Survey: Linear regression

Number of strata = 1
 Number of PSUs = 424

Number of obs = 424
 Population size = 408.1418
 Design df = 423
 F(0, 423) = .
 Prob > F = .
 R-squared = 0.0000

morethanone	Coefficient	Linearized std. err.	t	P> t	[95% conf. interval]	
_cons	.8704881	.0189293	45.99	0.000	.833281	.9076953

(running **regress** on estimation sample)

Survey: Linear regression

Number of strata = 1
 Number of PSUs = 418

Number of obs = 418
 Population size = 402.9395
 Design df = 417
 F(0, 417) = .
 Prob > F = .
 R-squared = 0.0000

morethanone	Coefficient	Linearized std. err.	t	P> t	[95% conf. interval]	
_cons	.7713327	.0228011	33.83	0.000	.7265133	.816152

124 postclose `memhold`

125 svy: reg morethanone
 (running **regress** on estimation sample)

Survey: Linear regression

Number of strata = 1
 Number of PSUs = 1,365

Number of obs = 1,365
 Population size = 1,368.8991
 Design df = 1,364
 F(0, 1364) = .
 Prob > F = .
 R-squared = 0.0000

morethanone	Coefficient	Linearized std. err.	t	P> t	[95% conf. interval]	
_cons	.8443039	.0111789	75.53	0.000	.8223742	.8662337

```

126
127 set scheme slmono
128 preserve
129 use morethanone_any, clear
130 set obs 6
    Number of observations (N) was 5, now 6.
131 replace fivegroups = 0 in 6
    (1 real change made)
132 replace propagree = .8443039 in 6
    (1 real change made)
133 replace seprop = .0111789 in 6
    (1 real change made)
134 lab def fivegroups 0 "All Rs" 1"Asian" 2"Black" 3"Latino" 4"White DEM" 5"White GOP"
135 lab val fivegroups fivegroups
136 gen UB = propagree + 1.96*seprop
137 gen LB = propagree - 1.96*seprop
138 twoway (bar propagree fivegroups, fcolor(gs8)) (rcap UB LB fivegroups, lcolor(black)
    > ), xlabel(, valuelabel) xtitle(" ") legend(off) ylabel(0(.25)1) title("(a) Proportio
    > n Agree with" ">1 Factor") name(morethanone, replace)
139 restore
140
141 tempname memhold
142 tempfile biopol
143 postfile `memhold' fivegroups propagree seprop using biopol, replace
    (file biopol.dta not found)
144 forval v=1/5 {
    2.         svy: reg YES_biopol if fivegroups==`v'
    3.         post `memhold' (`v') (_b[_cons]) (_se[_cons])
    4. }
    (running regress on estimation sample)

```

Survey: Linear regression

Number of strata = 1	Number of obs = 55
Number of PSUs = 55	Population size = 66.3357
	Design df = 54
	<u>F(0, 54)</u> = .
	Prob > F = .
	R-squared = 0.0000

YES_biopol	Linearized		t	P> t	[95% conf. interval]	
	Coefficient	std. err.				
<u>_cons</u>	.6962646	.0721858	9.65	0.000	.5515409	.8409883

(running **regress** on estimation sample)

Survey: Linear regression

Number of strata = 1
 Number of PSUs = 178

Number of obs = 178
 Population size = 185.3122
 Design df = 177
 F(0, 177) = .
 Prob > F = .
 R-squared = 0.0000

YES_biopol	Coefficient	Linearized std. err.	t	P> t	[95% conf. interval]	
_cons	.6784642	.0380052	17.85	0.000	.6034625	.753466

(running **regress** on estimation sample)

Survey: Linear regression

Number of strata = 1
 Number of PSUs = 48

Number of obs = 48
 Population size = 62.3657
 Design df = 47
 F(0, 47) = .
 Prob > F = .
 R-squared = 0.0000

YES_biopol	Coefficient	Linearized std. err.	t	P> t	[95% conf. interval]	
_cons	.7533757	.0800144	9.42	0.000	.5924074	.9143439

(running **regress** on estimation sample)

Survey: Linear regression

Number of strata = 1
 Number of PSUs = 424

Number of obs = 424
 Population size = 408.1418
 Design df = 423
 F(0, 423) = .
 Prob > F = .
 R-squared = 0.0000

YES_biopol	Coefficient	Linearized std. err.	t	P> t	[95% conf. interval]	
_cons	.4501509	.0275358	16.35	0.000	.3960268	.504275

(running **regress** on estimation sample)

Survey: Linear regression

Number of strata = 1
 Number of PSUs = 417

Number of obs = 417
 Population size = 402.3965
 Design df = 416
 F(0, 416) = .
 Prob > F = .
 R-squared = 0.0000

YES_biopol	Coefficient	Linearized std. err.	t	P> t	[95% conf. interval]	
_cons	.481445	.0264701	18.19	0.000	.4294133	.5334768

```
145 postclose `memhold'
```

```
146 svy: reg YES_biopol
      (running regress on estimation sample)
```

```
Survey: Linear regression
```

```
Number of strata =      1
Number of PSUs   = 1,364
Number of obs    =      1,364
Population size  = 1,368.3561
Design df       =      1,363
F(0, 1363)      =          .
Prob > F        =          .
R-squared       =      0.0000
```

YES_biopol	Coefficient	Linearized std. err.	t	P> t	[95% conf. interval]	
_cons	.5450189	.0152015	35.85	0.000	.5151981	.5748398

```
147
```

```
148 preserve
```

```
149 use biopol, clear
```

```
150 set obs 6
```

```
Number of observations (_N) was 5, now 6.
```

```
151 replace fivegroups = 0 in 6
```

```
(1 real change made)
```

```
152 replace propagree = .5450189 in 6
```

```
(1 real change made)
```

```
153 replace seprop = .0152015 in 6
```

```
(1 real change made)
```

```
154 lab def fivegroups 0 "All Rs" 1"Asian" 2"Black" 3"Latino" 4"White DEM" 5"White GOP"
```

```
155 lab val fivegroups fivegroups
```

```
156 gen UB = propagree + 1.96*seprop
```

```
157 gen LB = propagree - 1.96*seprop
```

```
158 twoway (bar propagree fivegroups, fcolor(gs8)) (rcap UB LB fivegroups, lcolor(black)
> ), xlabel(, valuelabel) xtitle(" ") legend(off) ylabel(0(.25)1) title("(b) Proportio
> n Agree with" "Biology and Policies") name(biopol, replace)
```

```
159 restore
```

```
160
```

```
161 graph combine morethanone biopol, ycommon row(1) altshrink ysize(2.5) xsize(6.5)
```

```
162 graph export AppendixFigureC2.pdf, replace
file AppendixFigureC2.pdf saved as PDF format
```

```
163
```

```
164 *****N's for caption*****
```

165 sum morethanone YES_biopol

Variable	Obs	Mean	Std. dev.	Min	Max
morethanone	1,446	.8416321	.3652119	0	1
YES_biopol	1,445	.5287197	.4993473	0	1

166 tab morethanone fivegroup

RECODE of diff_agree (NOT_bio NOT_cul NOT_pol == 0)	Asian	Black	fivegroups Hispanic	White DEM	White GOP	Total
0	7	21	5	60	99	192
1	49	170	43	390	349	1,001
Total	56	191	48	450	448	1,193

167 tab YES_biopol fivegroups

YES_biopol	Asian	Black	fivegroups Hispanic	White DEM	White GOP	Total
0	22	63	10	256	228	579
1	34	128	38	194	219	613
Total	56	191	48	450	447	1,192

168

169 *****END FIGURE 2*****

170 *****cleaning up directory*****

171 erase morethanone_any.dta

172 erase biopol.dta

173 *****cleaning up directory*****

174

175 log close

name: <unnamed>

log: C:\Users\kamcd\Dropbox\CDK WORK\racial disparities essentialism\JOP repli

> cation files\Anoll Kam Marcellin ANES 2022 Pilot Analyses.smcl

log type: smcl

closed on: 10 Jan 2025, 13:26:36